



SEQUENCE LISTING

<110> Boylan, John  
Bowers, Alex

<120> Novel Serine Threonine Kinase Member, h2520-59

<130> 01017/36524A

<140> US/09/909,474

<141> 2001-07-19

<150> US 60/219,204

<151> 2000-07-19

<160> 15

<170> PatentIn version 3.0

<210> 1

<211> 2059

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (49)..(1122)

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Thr Pro Leu Ala Ala Pro Ala Gly Ser Leu Ser Arg Lys Lys Arg Leu  
5 10 15

gag ttg gat gac aac tta gat acc gag cgt ccc gtc cag aaa cga gct 153  
Glu Leu Asp Asp Asn Leu Asp Thr Glu Arg Pro Val Gln Lys Arg Ala  
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cga agt ggg ccc cag ccc aga ctg ccc ccc tgc ctg ttg ccc ctg agc 201  
Arg Ser Gly Pro Gln Pro Arg Leu Pro Pro Cys Leu Leu Pro Leu Ser  
40 45 50

cca cct act gct cca gat cgt gca act gct gtg gcc act gcc tcc cgt 249  
Pro Pro Thr Ala Pro Asp Arg Ala Thr Ala Val Ala Thr Ala Ser Arg  
55 60 65

ctt ggg ccc tat gtc ctc ctg gag ccc gag gag ggc ggg cgg gcc tac 297  
Leu Gly Pro Tyr Val Leu Leu Glu Pro Glu Glu Gly Gly Arg Ala Tyr  
70 75 80

cgg gcc ctg cac tgc cct aca ggc act gag tat acc tgc aag gtg tac 345  
Arg Ala Leu His Cys Pro Thr Gly Thr Glu Tyr Thr Cys Lys Val Tyr  
85 90 95

ccc gtc cag gaa gcc ctg gcc gtg ctg gag ccc tac gcg cgg ctg ccc 393  
Pro Val Gln Glu Ala Leu Ala Val Leu Glu Pro Tyr Ala Arg Leu Pro  
100 105 110 115

RECEIVED

APR 22 2002

TECH CENTER 1600/2900

B1

ccg cac aag cat gtg gct cgg ccc act gag gtc ctg gct ggt acc cag	441
Pro His Lys His Val Ala Arg Pro Thr Glu Val Leu Ala Gly Thr Gln	
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ctc ctc tac gcc ttt ttc act cgg acc cat ggg gac atg cac agc ctg	489
Leu Leu Tyr Ala Phe Phe Thr Arg Thr His Gly Asp Met His Ser Leu	
135 140 145	
gtg cga agc cgc cac cgt atc cct gag cct gag gct gcc gtg ctc ttc	537
Val Arg Ser Arg His Arg Ile Pro Glu Pro Glu Ala Ala Val Leu Phe	
150 155 160	
cgc cag atg gcc acc gcc ctg gcg cac tgt cac cag cac ggt ctg gtc	585
Arg Gln Met Ala Thr Ala Leu Ala His Cys His Gln His Gly Leu Val	
165 170 175	
ctg cgt gat ctc aag ctg tgt cgc ttt gtc ttc gct gac cgt gag agg	633
Leu Arg Asp Leu Lys Leu Cys Arg Phe Val Phe Ala Asp Arg Glu Arg	
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aag aag ctg gtg ctg gag aac ctg gag gac tcc tgc gtg ctg act ggg	681
Lys Lys Leu Val Leu Glu Asn Leu Glu Asp Ser Cys Val Leu Thr Gly	
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Pro Asp Asp Ser Leu Trp Asp Lys His Ala Cys Pro Ala Tyr Val Gly	
215 220 225	
cct gag ata ctc agc tca cgg gcc tca tac tgc ggc aag gca gcc gat	777
Pro Glu Ile Leu Ser Ser Arg Ala Ser Tyr Ser Gly Lys Ala Ala Asp	
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Val Trp Ser Leu Gly Val Ala Leu Phe Thr Met Leu Ala Gly His Tyr	
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ccc ttc cag gac tgc gag cct gtc ctg ctc ttc ggc aag atc cgc cgc	873
Pro Phe Gln Asp Ser Glu Pro Val Leu Leu Phe Gly Lys Ile Arg Arg	
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Gly Ala Tyr Ala Leu Pro Ala Gly Leu Ser Ala Pro Ala Arg Cys Leu	
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gtt cgc tgc ctc ctt cgt cgg gag cca gct gaa cgg ctc aca gcc aca	969
Val Arg Cys Leu Leu Arg Arg Glu Pro Ala Glu Arg Leu Thr Ala Thr	
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Gly Ile Leu Leu His Pro Trp Leu Arg Gln Asp Pro Met Pro Leu Ala	
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Pro Thr Arg Ser His Leu Trp Glu Ala Ala Gln Val Val Pro Asp Gly	
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Leu Gly Leu Asp Glu Ala Arg Glu Glu Glu Gly Asp Arg Glu Val Val	
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ctg tat ggc taggaccacc ctactacacg ctacagctgcc aacagtggat	1162
Leu Tyr Gly	

B1  
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tgagtttggg ggtagctcca agccttctcc tgcctctgaa ctgagccaaa ccttcagtgc	1222
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 <213> Homo sapiens

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20 25 30

Lys Arg Ala Arg Ser Gly Pro Gln Pro Arg Leu Pro Pro Cys Leu Leu
35 40 45

Pro Leu Ser Pro Pro Thr Ala Pro Asp Arg Ala Thr Ala Val Ala Thr
50 55 60

Ala Ser Arg Leu Gly Pro Tyr Val Leu Leu Glu Pro Glu Glu Gly Gly
65 70 75 80

Arg Ala Tyr Arg Ala Leu His Cys Pro Thr Gly Thr Glu Tyr Thr Cys
85 90 95

B1  
Cont.

Lys Val Tyr Pro Val Gln Glu Ala Leu Ala Val Leu Glu Pro Tyr Ala  
 100 105 110  
 Arg Leu Pro Pro His Lys His Val Ala Arg Pro Thr Glu Val Leu Ala  
 115 120 125  
 Gly Thr Gln Leu Leu Tyr Ala Phe Phe Thr Arg Thr His Gly Asp Met  
 130 135 140  
 His Ser Leu Val Arg Ser Arg His Arg Ile Pro Glu Pro Glu Ala Ala  
 145 150 155 160  
 Val Leu Phe Arg Gln Met Ala Thr Ala Leu Ala His Cys His Gln His  
 165 170 175  
 Gly Leu Val Leu Arg Asp Leu Lys Leu Cys Arg Phe Val Phe Ala Asp  
 180 185 190  
 Arg Glu Arg Lys Lys Leu Val Leu Glu Asn Leu Glu Asp Ser Cys Val  
 195 200 205  
 Leu Thr Gly Pro Asp Asp Ser Leu Trp Asp Lys His Ala Cys Pro Ala  
 210 215 220  
 Tyr Val Gly Pro Glu Ile Leu Ser Ser Arg Ala Ser Tyr Ser Gly Lys  
 225 230 235 240  
 Ala Ala Asp Val Trp Ser Leu Gly Val Ala Leu Phe Thr Met Leu Ala  
 245 250 255  
 Gly His Tyr Pro Phe Gln Asp Ser Glu Pro Val Leu Leu Phe Gly Lys  
 260 265 270  
 Ile Arg Arg Gly Ala Tyr Ala Leu Pro Ala Gly Leu Ser Ala Pro Ala  
 275 280 285  
 Arg Cys Leu Val Arg Cys Leu Leu Arg Arg Glu Pro Ala Glu Arg Leu  
 290 295 300  
 Thr Ala Thr Gly Ile Leu Leu His Pro Trp Leu Arg Gln Asp Pro Met  
 305 310 315 320  
 Pro Leu Ala Pro Thr Arg Ser His Leu Trp Glu Ala Ala Gln Val Val  
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 Pro Asp Gly Leu Gly Leu Asp Glu Ala Arg Glu Glu Glu Gly Asp Arg  
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Glu Val Val Leu Tyr Gly  
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 Lys Arg Leu Glu Leu Asp Asp Asn Leu Asp Thr Glu Arg Pro Val Gln  
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 Lys Arg Ala Arg Ser Gly Pro Gln Pro Arg Leu Pro Pro Cys Leu Leu  
 35 40 45  
 Pro Leu Ser Pro Pro Thr Ala Pro Asp Arg Ala Thr Ala Val Ala Thr  
 50 55 60  
 Ala Ser Arg Leu Gly Pro Tyr Val Leu Leu Glu Pro Glu Glu Gly Gly  
 65 70 75 80  
 Arg Ala Tyr Gln Ala Leu His Cys Pro Thr Gly Thr Glu Tyr Thr Cys  
 85 90 95  
 Lys Val Tyr Pro Val Gln Glu Ala Pro Ala Val Leu Glu Pro Tyr Ala  
 100 105 110  
 Arg Leu Pro Pro His Lys His Val Ala Arg Pro Thr Glu Val Leu Ala  
 115 120 125  
 Gly Thr Gln Leu Leu Tyr Ala Phe Phe Thr Arg Thr His Gly Asp Met  
 130 135 140  
 His Ser Leu Val Arg Ser Arg His Arg Ile Pro Glu Pro Glu Ala Ala  
 145 150 155 160  
 Val Leu Phe Arg Gln Met Ala Thr Ala Leu Ala His Cys His Gln His  
 165 170 175  
 Gly Leu Val Leu Arg Asp Leu Lys Leu Cys Arg Phe Val Phe Ala Asp  
 180 185 190  
 Arg Glu Arg Lys Lys Leu Val Leu Glu Asn Leu Glu Asp Ser Cys Val  
 195 200 205  
 Leu Thr Gly Pro Asp Asp Ser Leu Trp Asp Lys His Ala Cys Pro Ala  
 210 215 220  
 Tyr Val Gly Pro Glu Ile Leu Ser Ser Arg Ala Ser Tyr Ser Gly Lys  
 225 230 235 240  
 Ala Ala Asp Val Trp Ser Leu Gly Val Ala Leu Phe Thr Met Leu Ala  
 245 250 255  
 Gly His Tyr Pro Phe Gln Asp Ser Glu Pro Val Leu Leu Phe Gly Lys  
 260 265 270  
 Ile Arg Arg Gly Ala Tyr Ala Leu Pro Ala Gly Leu Ser Ala Pro Ala  
 275 280 285  
 Arg Cys Leu Val Arg Cys Leu Leu Arg Arg Glu Pro Ala Glu Arg Leu  
 290 295 300

B1  
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Thr Ala Thr Gly Ile Leu Leu His Pro Trp Leu Arg Gln Asp Pro Met  
 305 310 315 320

Pro Leu Ala Pro Thr Arg Ser His Leu Trp Glu Ala Ala Gln Val Val  
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Pro Asp Gly Leu Gly Leu Asp Glu Ala Arg Glu Glu Glu Gly Asp Arg  
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Glu Val Val Leu Tyr Gly  
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Gln Arg Lys Trp Arg Arg Leu Arg Ala Arg Pro Leu Leu Gly Pro Gly  
 20 25 30

Gln Gly Trp Ser Trp Ala Gly Ile Pro Ser Ser Ala Ala Ala Gln Arg  
 35 40 45

Ala Gly Pro Pro Ala Gly Ala Leu Glu Ala Leu Ser Pro Gly Gly Ala  
 50 55 60

Arg Ala His Ala Glu Arg Arg Gly Glu Met Arg Ala Thr Pro Leu Ala  
 65 70 75 80

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Ala Pro Ala Gly Ser Leu Ser Arg Lys Lys Arg Leu Glu Leu Asp Asp  
85 90 95

Asn Leu Asp Thr Glu Arg Pro Val Gln Lys Arg Ala Arg Ser Gly Pro  
100 105 110

Gln Pro Arg Leu Pro Pro Cys Leu Leu Pro Leu Ser Pro Pro Thr Ala  
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Pro Asp Arg Ala Thr Ala Val Xaa Thr Xaa Ser Arg Xaa Xaa Xaa Tyr  
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Val Leu Leu Glu Ala Arg Arg Xaa Ala  
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<210> 10  
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Gly Pro Gly Trp Tyr Pro Ala Pro Leu Arg Leu Phe His Ser Asp Pro  
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20 25 30

Glu Ala Ala Val Leu Phe Arg Gln Met Ala Thr Ala Leu Ala His Cys  
35 40 45

His Gln His Gly Leu Val Leu Arg Asp Leu Lys Leu Cys Arg Phe Val  
50 55 60

Phe Ala Asp Arg Glu Arg Lys Lys Leu Val Leu Glu Asn Leu Glu Asp  
65 70 75 80

Ser Cys Val Leu Thr Gly Pro Asp Asp Ser Leu Trp Asp Lys His Ala  
85 90 95

Cys Pro Ala Tyr Val Gly Pro Glu Ile Leu Ser Ser Arg Ala Ser Tyr  
100 105 110

Ser Gly Lys Ala Ala Asp Val Trp Ser Leu Gly Val Ala Leu Phe Thr  
115 120 125

Met Leu Ala Gly His Tyr Pro Phe Gln Asp Ser Glu Pro Val Leu Leu  
130 135 140

Phe Gly Lys Ile Arg Arg Gly Ala Tyr Ala Leu Pro Ala Gly Leu Ser  
145 150 155 160

Ala Pro Ala Arg Cys Leu Val Arg Cys Leu Leu Arg Arg Glu Pro Ala  
165 170 175

Glu Arg Leu Thr Ala Thr Gly Ile Leu Leu His Pro Trp Leu Arg Gln  
180 185 190

Asp Pro Met Pro Leu Ala Pro Thr Arg Ser His Leu Trp Glu Ala Ala  
195 200 205

Gln Val Val Pro Asp Gly Leu Gly Leu Asp Glu Ala Arg Glu Glu Glu  
210 215 220

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Cont.



Gly Asp Arg Glu Val Val Leu Tyr Gly  
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<210> 11  
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<400> 11

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Arg Ala Gly Pro Pro Ala Gly Ala Leu Glu Ala Leu Ser Pro Gly Gly  
20 25 30

Ala Arg Ala His Ala Glu Arg Arg Gly Glu Met Arg Ala Thr Pro Leu  
35 40 45

Ala Ala Pro Ala Gly Ser Leu Ser Arg Lys Lys Arg Leu Glu Leu Asp  
50 55 60

Asp Asn Leu Asp Thr Glu Arg Pro Val Gln Lys Arg Ala Arg Ser Gly  
65 70 75 80

Pro Gln Pro Arg Leu Pro Pro Cys Leu Leu Pro Leu Ser Pro Pro Thr  
85 90 95

Ala Pro Asp Arg Ala Thr Ala Val Ala Thr Ala Ser Arg Leu Gly Pro  
100 105 110

Tyr Val Leu Leu Glu Pro Glu Glu Gly Gly Arg Ala Tyr Gln Ala Leu  
115 120 125

His Cys Pro Thr Gly Thr Glu Tyr Thr Cys Lys Val Tyr Pro Val Gln  
130 135 140

Glu Ala Leu Ala Val Leu Glu Pro Tyr Ala Arg Leu Pro Pro His Lys  
145 150 155 160

His Val Ala Arg Pro Thr Glu Val Leu Ala Gly Thr Gln Leu Leu Tyr  
165 170 175

Ala Phe Phe Thr Arg Thr His Gly Asp Met His Ser Leu Val Arg Ser  
180 185 190

Arg His Arg Ile Pro Glu Pro Glu Ala Ala Val Leu Phe Arg Gln Met  
195 200 205

Ala Thr Ala Leu Ala His Cys His Gln His Gly Leu Val Leu Arg Asp  
210 215 220

Leu Lys Leu Cys Arg Phe Val Phe Ala Asp Arg Glu Arg Lys Lys Leu  
225 230 235 240

Val Leu Glu Asn Leu Glu Asp Ser Cys Val Leu Thr Gly Pro Asp Asp  
245 250 255

Ser Leu Trp Asp Lys His Ala Cys Pro Ala Tyr Val Gly Pro Glu Ile  
260 265 270

Leu Ser Ser Arg Ala Ser Tyr Ser Gly Lys Ala Ala Asp Val Trp Ser  
275 280 285

B1  
Cont.

Leu Gly Val Ala Leu Phe Thr Met Leu Ala Gly His Tyr Pro Phe Gln  
290 295 300

Asp Ser Glu Pro Val Leu Leu Phe Gly Lys Ile Arg Arg Gly Ala Tyr  
305 310 315 320

Ala Leu Pro Ala Gly Leu Ser Ala Pro Ala Arg Cys Leu Val Arg Cys  
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Leu Leu Arg Arg Glu Pro Ala Glu Arg Leu Thr Ala Thr Gly Ile Leu  
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Leu His Pro Trp Leu Arg Gln Asp  
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gacctgagat actcagctca cgggcctcat actcgggcaa ggcagccgat gtctggagcc 180  
tgggcgtggc gctcttcacc atgctggccg gccactaccc cttccaggac tcggagcctg 240  
tcttgctctt cggcaagatc cgccgcgggg cctacgcctt gcctgcagge ctctcggccc 300  
ctgcccgtg tctggttcgc tgccctcttc gtcgggagcc agctgaacgg ctcacagcca 360  
caggcatcct cctgcacccc tggctgcgac aggaccgat gcccttagcc ccaaccgat 420  
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Arg Ser Gly Pro Gln Pro Arg Leu Cys  
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<212> PRT  
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<400> 14

Gly Pro Tyr Val Leu Leu Glu Pro Glu Gly Gly Arg Ala Tyr Gln  
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Ala Leu His Cys Pro Thr Gly Thr Glu  
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<210> 15

<211> 25

<212> PRT

<213> Homo sapiens

<400> 15

Arg Ser His Leu Trp Glu Ala Ala Gln Val Val Pro Asp Gly Leu Gly  
1 5 10 15

Leu Asp Glu Ala Arg Glu Glu Glu Cys  
20 25

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